

Resource Summary Report

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DNA Methylation Age Calculator

RRID:SCR_026822

Type: Tool

Proper Citation

DNA Methylation Age Calculator (RRID:SCR_026822)

Resource Information

URL: <https://dnamage.genetics.ucla.edu/>

Proper Citation: DNA Methylation Age Calculator (RRID:SCR_026822)

Description: Web portal contains information on how to calculate DNA methylation (DNAm) age based on data measured using the Illumina Infinium platform.

Resource Type: portal, web service, data or information resource, data access protocol, software resource

Keywords: calculate DNA methylation age, DNAm age, Illumina Infinium data,

Availability: Restricted

Resource Name: DNA Methylation Age Calculator

Resource ID: SCR_026822

Record Creation Time: 20250419T055109+0000

Record Last Update: 20260815T042924+0000

Ratings and Alerts

No rating or validation information has been found for DNA Methylation Age Calculator.

No alerts have been found for DNA Methylation Age Calculator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Chen Y, et al. (2026) Life-course Psychosocial Adversity and Biological Aging in the Hispanic Community Health Study / Study of Latinos: A Life-course Model Analysis. Research square.

Pirini F, et al. (2025) Comprehensive genetic and epigenetic characterization of Lynch-like syndrome patients. International journal of cancer, 157(4), 788.

Hasselholm EB, et al. (2025) Epigenetic age acceleration in Turner and Klinefelter syndrome: Correlations with clinical aging markers. Clinical epigenetics, 17(1), 147.

Bejaoui Y, et al. (2025) The role of protective genetic variants in modulating epigenetic aging. GeroScience, 47(4), 5995.

Janssens GE, et al. (2025) Nutritional associations with decelerated epigenetic aging: vegan diet in a Dutch population. Clinical epigenetics, 17(1), 133.

Sandhar B, et al. (2025) Heterogeneity of thymic output in the elderly and its association with sex and smoking. JCI insight, 10(15).

Fries GR, et al. (2025) Association between epigenetic aging acceleration and amyloid biomarkers in bipolar disorder. medRxiv : the preprint server for health sciences.

Gampawar P, et al. (2025) Epigenetic age acceleration is related to cognitive decline in the elderly: Results of the Austrian Stroke Prevention Study. Psychiatry and clinical neurosciences, 79(5), 229.

Villanueva JL, et al. (2025) Dietary associations with reduced epigenetic age: a secondary data analysis of the methylation diet and lifestyle study. Aging, 17(4), 994.

Zhao X, et al. (2025) PTSD and epigenetic aging: a longitudinal meta-analysis. Psychological medicine, 55, e142.

Newman BT, et al. (2025) Epigenetic age acceleration predicts subject-specific white matter degeneration in the human brain. Aging cell, 24(4), e14426.

Jiang X, et al. (2025) Identification of blood-derived DNA methylation biomarkers of glaucoma and intraocular pressure measurements in three European ancestry cohorts including the Canadian longitudinal study on aging. Epigenetics, 20(1), 2566496.

Pusparum M, et al. (2025) From ageing clocks to human digital twins in personalising healthcare through biological age analysis. NPJ digital medicine, 8(1), 537.

Xu EY, et al. (2025) Epigenetic and Structural Brain Aging and Their Associations With Major Depressive Disorder. Biological psychiatry global open science, 5(6), 100577.

Kwiatkowska KM, et al. (2024) B Cells Isolated from Individuals Who Do Not Respond to the HBV Vaccine Are Characterized by Higher DNA Methylation-Estimated Aging Compared to Responders. Vaccines, 12(8).

Dawangpa A, et al. (2024) Impact of combined exercise on blood DNA methylation and physical health in older women with obesity. PloS one, 19(12), e0315250.

Philibert R, et al. (2024) Objective Assessments of Smoking and Drinking Outperform Clinical Phenotypes in Predicting Variance in Epigenetic Aging. Genes, 15(7).

Miao K, et al. (2024) Five years of change in adult twins: longitudinal changes of genetic and environmental influence on epigenetic clocks. BMC medicine, 22(1), 289.

Sabbatinelli J, et al. (2024) DNA Methylation-derived biological age and long-term mortality risk in subjects with type 2 diabetes. Cardiovascular diabetology, 23(1), 250.

Kawamura T, et al. (2024) Healthy Japanese dietary pattern is associated with slower biological aging in older men: WASEDA'S health study. Frontiers in nutrition, 11, 1373806.